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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/846,456	05/02/2001	Marie-Francoise Rosier-Montus	3806.0505	1457
5487	7590	04/05/2006	EXAMINER	
			SULLIVAN, DANIEL M	
		ART UNIT		PAPER NUMBER
		1636		
DATE MAILED: 04/05/2006				

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/846,456	ROSIER-MONTUS ET AL.	
	Examiner	Art Unit	
	Daniel M. Sullivan	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) Responsive to communication(s) filed on 17 January 2006.
- 2a) This action is FINAL. 2b) This action is non-final.
- 3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) Claim(s) 1-3,5-14,23,33-38,57 and 58 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) Claim(s) 1,35,36 and 58 is/are allowed.
- 6) Claim(s) 2,3,5-14,23,33,34,37 and 38 is/are rejected.
- 7) Claim(s) 57 is/are objected to.
- 8) Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) The specification is objected to by the Examiner.
- 10) The drawing(s) filed on _____ is/are: a) accepted or b) objected to by the Examiner.
 Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
 Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
 - a) All b) Some * c) None of:
 1. Certified copies of the priority documents have been received.
 2. Certified copies of the priority documents have been received in Application No. _____.
 3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) Notice of References Cited (PTO-892)
- 2) Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
 Paper No(s)/Mail Date _____.
- 4) Interview Summary (PTO-413)
 Paper No(s)/Mail Date. _____.
- 5) Notice of Informal Patent Application (PTO-152)
- 6) Other: Sequence alignments.

DETAILED ACTION

This Office Action is a reply to the Paper filed 17 January 2006 in response to the Final Office Action mailed 17 May 2005. Claims 1-3 and 5-38 were considered in the 17 May Office Action. Claims 15-22 and 24-32 were canceled, claims 1-3, 5, 6 and 23 were amended, and claims 57-58 were added in the 17 January Paper.

Continued Examination Under 37 CFR 1.114

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 17 January 2006 has been entered.

Presently, claims 1-3, 5-14, 23, 33-38, 57 and 58 are pending and under consideration.

Response to Amendment

Rejection of claims 15-22 and 24-32 is rendered moot by the cancellation thereof.

Claim Rejections - 35 USC § 112

Rejection of claim 23 under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement for the reasons set forth in the 17 May Office Action is withdrawn in view of the fact that the claim does not require that the nucleic acid exhibit transcriptional regulatory activity.

Rejection of claims 1-3, 5-14, 23, 33-38, 57 and 58 under 35 U.S.C. 112, second paragraph, as being indefinite is withdrawn in view of the amendments to the claims.

New Grounds

Claim Objections

Claim 57 is objected to because of the following informalities: The claim is objected to because the phrase “a polynucleotide which has having at least...” is grammatically incorrect. Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 37 and 38 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. The discussion of “Recombinant host cells” in the specification commencing at page 4 does not provide a limiting definition of a host cell within the scope of the claims. In addition, the specification commencing on page 59 contemplates *in vivo* gene transfer of the nucleic acids of the invention and contemplates at page 74, line 10, *in vivo* gene transfer into human cells. Given that there is no limiting definition of a host cell and the application contemplates the production of recombinant host cells in humans *in vivo*, the host cell of the claims can reasonably be construed as encompassing a cell present or intended to be present in a human being, said cell becoming integrated into the human being and therefore being an

inseparable part of the human itself. The scope of the claim, therefore, encompasses a human being, which is non-statutory subject matter. As such, the recitation of the limitation “non-human” or “isolated host cell” would be remedial. See 1077 O.G. 24, April 21, 1987.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 7-12, 33 and 34 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 7-12 are indefinite in reciting, “said isolated nucleic acid is a polynucleotide comprising a sequence ranging from the nucleotide at position –1 to the nucleotide at position –200 [etc.], with respect to the first nucleotide transcribed, which is located at position 2894 of the nucleotide sequence of SEQ ID NO: 1.” First, there is no antecedent basis for “the nucleotide at position –1” or “the nucleotide at position –200 [etc.]” or a “first nucleotide transcribed” in the claims from which claims 7-12 depend. Although claim 6 recites, “said nucleic acid modifies the transcription of a polynucleotide placed under its control” the claim does not require that the nucleic acid actually comprise a polynucleotide placed under its control. Rather, claim 6 is reasonably construed as reciting a functional property of the claimed nucleic acid, but does not require that the claimed nucleic acid actually comprise an expression cassette. Therefore, there is no –1 position or “first nucleotide transcribed” inherent to the claims from which claims 7-12 depend. Furthermore, even if the prior claims were directed to an expression cassette comprising

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“a sequence ranging from...”, there is neither explicit nor implicit antecedent for a position -200, -600, -2894, -995, *etc.* in the claims.

In addition, it is unclear to what the “sequence ranging from the nucleotide at position [A] to the nucleotide at position [B]” is referring. Although the claim recites that the numbering is with respect to the first nucleotide transcribed, which is identified as being located at position 2894 of the nucleotide sequence of SEQ ID NO: 1, the claims do not appear to be limited to comprising the sequence of SEQ ID NO: 1. Claims 3 and 5, from which claim 6 and subsequent claims depend, are clearly not limited to comprising SEQ ID NO: 1. In view of this, it is unclear what sequence is comprised within the range recited in the claims, other than the sequence of claims 3 and 5, which can be as short as 20 or 35 nucleotides, respectively. Furthermore, as the claims are not limited to comprising SEQ ID NO: 1, it is unclear how the identification of position 2894 of SEQ ID NO: 1 as “the first nucleotide transcribed” limits the claim. In the absence of a limitation that the claim comprise SEQ ID NO: 1 or some significant portion of SEQ ID NO: 1 that includes the transcriptional start site, it is unclear how position 2894 of SEQ ID NO: 1 is related to the nucleic acid being claimed. This is because the transcriptional start site in SEQ ID NO: 1 is defined by the regulatory elements lying upstream of SEQ ID NO: 1, which are not necessarily comprised by the claimed nucleic acid unless it is Applicant’s intention that the identification of the first nucleotide transcribed as located at position 2894 of the nucleotide sequence SEQ ID NO: 1 limit the claimed nucleic acid to comprising the regulatory elements of SEQ ID NO: 1 configured so as to provide a first nucleotide transcribed at a position corresponding to position 2894 of SEQ ID NO: 1.

Given that the terms in the claims lack antecedent basis, the claims do not clearly indicate what sequence is comprised within the range recited in the claim and it is unclear how the recitation of the first nucleotide transcribed to being located at position 2894 of SEQ ID NO: 1 limits the claims, the metes and bounds of the claimed subject matter as a whole are unclear.

Claim 33 is indefinite in reciting that the polynucleotide encodes one compound chosen from “polypeptides of interest and nucleic acids of interest”. It is unclear whether the use of the plural requires that the nucleic acid encode more than one polypeptide or nucleic acid. If this were the case, then the requirement for multiple polypeptides or nucleic acids would seem inconsistent with the phrase “at least one”. If it is Applicant’s intention that the claims cover the nucleic acid encoding at least one polypeptide or at least one nucleic acid, it would be remedial to amend the claims to recite the singular “polypeptide” and “nucleic acid”, which are construed as encompassing one or more.

Claim 34 is indefinite insofar as it depends from claim 33.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

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Claims 2, 3, 5-14 and 23 are rejected under 35 U.S.C. 102(b) as being anticipated by Langmann et al. (Biochemical and biophysical Research Communication, 2/9/1999, Vol. 257:29-33; see the entire document).

As stated in the 19 November 2002 Office Action, Langmann et al teach the purification and characterization of a full-length cDNA (~6.8 kb) for the human ABC1 transporter that was given the accession number AJ012376 (e.g. Abstract; page 30, 1st paragraph Results and Discussion). The attached NCBI readout for AJ012376 indicates that the full-length cDNA taught by Langmann et al comprises the first 120 nucleotides 5' of the coding sequence. This 5' coding sequence would necessarily "modify" the transcription of the coding sequence under its control.

This rejection was originally made in the 19 November Office Action and withdrawn when the claims were limited to comprising a polynucleotide having at least 300 nucleotides of SEQ ID NO: 1 (see Applicant's remarks filed 21 April 2003, first full paragraph on page 11). In the 17 January Paper, Applicant has amended the claims such that they are no longer limited to comprising 500 or more consecutive nucleotides of SEQ ID NO: 1. Therefore, the claimed subject matter again embraces the nucleic acid of Langmann *et al.* and the claims are properly rejected under 35 USC §102(b) as anticipated by Langmann *et al.*

Claim 2 is rejected under 35 U.S.C. 102(b) as being anticipated by Auffray et al (C. R. Acad. Sci. III, Sci. Vie 318, No. 2, pages 263-272; see the search reports attached to the 19 November Office Action action).

As stated in the 19 November Office Action, as indicated by the attached search reports, Auffray et al teach the sequence the sequence of a cDNA clone obtained from the infant brain. The sequence taught by Auffray et al comprises greater than 20 contiguous nucleotides of SEQ ID NO: 2.

This rejection was originally made in the 19 November Office Action and maintained in the Office Action mailed 12 November 2003 on the grounds that the phrase "...comprising a polynucleotide of the sequence SEQ ID NO: 2..." can be read broadly to specify any sequence found within SEQ ID NO: 2 (see page 3 of the 12 November Office Action). The rejection was subsequently withdrawn when the claims were amended to recite, "...a polynucleotide of the entire nucleotide sequence..." However, the 17 January Paper amends the claims such that this phrase is no longer recited in claim 2 and the claim again embraces the nucleic acid of Auffray *et al.* Therefore, the claims are properly rejected under 35 USC §102(b) as anticipated by Auffray *et al.*

Claims 2, 3, 6-14 and 23 are rejected under 35 U.S.C. 102(e) as being anticipated by Tall U.S. Patent No. 6,773,893 B1.

Claim 1 of Tall is directed to an isolated ABC1 promoter that directs transcription of a heterologous coding sequence positioned downstream therefrom, wherein the promoter comprises nucleotides having the nucleotide sequence beginning at bp 624 and ending at bp 1197 of SEQ ID NO: 1 or beginning at bp 1005 and ending at bp 1059 of SEQ ID NO: 1. As evidenced by the sequence alignments mailed herewith (us-09-846-456a-1.mi, RESULT 3 and us-09-846-456a-3.rni, RESULT 3), the claimed nucleic acids of Tall anticipate the nucleic acid

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comprising a nucleotide sequence of SEQ ID NO: 2 and comprising at least 20 consecutive nucleotides of SEQ ID NO: 3 according to claims 2 and 3. Furthermore, claim 1 of Tall recites that the nucleic acid directs transcription according to the instant claims 6-12 and comprises various regulatory elements identified in the instant application as having positive or negative regulatory activity according to claims 13 and 14 (see especially Figure 2 and Table 1 of the instant application, which identifies several regulatory elements, and the sequence alignment us-09-846-456a-3.rni, page 4, which shows where the identified elements appear in the sequence of Tall). Finally, given the close structural similarity of the nucleic acid claimed by Tall to the instant SEQ ID NO: 1, one would expect, absent evidence to the contrary, that the nucleic acid of Tall would hybridize to a nucleic acid having 500 or more consecutive nucleotides of the sequence complementary to SEQ ID NO: 1.

The nucleic acid of Tall is the same as the nucleic acid of the instant claims. Therefore, the claims are properly rejected under 35 USC §102(e) as anticipated by Tall.

Claims 2, 5, 6-13 and 23 are rejected under 35 U.S.C. 102(e) as being anticipated by Hayden *et al.* U.S. Patent No. 6,617,122 B1.

Hayden *et al.* teaches a nucleic acid comprising the ABC1 promoter, which nucleic acid comprises SEQ ID NO: 14 (see especially Figure 12 and the brief description thereof at column 12, lines 19-21). As evidenced by the sequence alignments mailed herewith (us-09-846-456a-2.mi, RESULT 1 and us-09-846-456a-5.rni, RESULT 9), the nucleic acid of Hayden *et al.* anticipates the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 2 and comprising at least 35 consecutive nucleotides of SEQ ID NO: 5 according to claims 2 and 5. Furthermore,

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Hayden *et al.* teaches that the nucleic acid is a promoter according to the instant claims 6-13.

Finally, given the close structural similarity of the nucleic acid of Hayden *et al.* to nucleic acids comprised within the instant SEQ ID NO: 1, one would expect, absent evidence to the contrary, that the nucleic acid of Hayden *et al.* would hybridize to a nucleic acid having 500 or more consecutive nucleotides of the sequence complementary to SEQ ID NO: 1 according to the instant claim 23.

The nucleic acids of Hayden *et al.* are the same as the nucleic acid of the instant claims.

Therefore, the claims are properly rejected under 35 USC §102(e) as anticipated by Hayden *et al.*

Allowable Subject Matter

Claims 1, 35, 36 and 58 are allowed.

Claim 57 is objected to.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Daniel M Sullivan whose telephone number is 571-272-0779. The examiner can normally be reached on Monday through Friday 6:30-3:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel, Ph.D. can be reached on 571-272-0781. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) (<http://pair-direct.uspto.gov>) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to

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midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days.

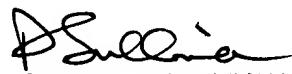
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Daniel M. Sullivan, Ph.D.

Primary Examiner

Art Unit 1636



DANIEL M. SULLIVAN
PATENT EXAMINER

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 06:52:37 ; Search time 45:2164 Seconds
(without alignment(s))
14034.494 Million cell updates/sec

Title: US-09-846-456A-2
Perfect score: 357
Sequence: 1 tggaggctctcagtcgtggagg.....gagggaaggaaactcgatgg 357

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs 888780828 residues

Total number of hits satisfying chosen parameters: 2600114

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0^t
Listing first 45 summaries

Database : Issued Patents NA:*

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9: /cn2_6/podata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	340.2	95.3	10545	US-09-526-193A-14	Sequence 14, Appl
2	203.8	57.1	10653	US-10-004489-101	Sequence 101, Appl
3	203.4	57.0	4475	US-09-6211-976-13889	Sequence 13889, A
4	159.4	44.6	10442	US-09-5956-141C-1	Sequence 1, Appl
5	159.4	44.6	10442	US-09-5956-526C-1	Sequence 1, Appl
6	159.4	44.6	10474	US-09-5956-141C-7	Sequence 7, Appl
7	159.4	44.6	10474	US-09-5956-141C-9	Sequence 9, Appl
8	159.4	44.6	10474	US-09-5956-526C-7	Sequence 7, Appl
9	159.4	44.6	10474	US-09-5956-526C-9	Sequence 9, Appl
10	135.8	38.0	7860	US-09-526-193A-2	Sequence 2, Appl
11	37.8	10.6	30678	US-09-949-016-1545	Sequence 15145, A
12	37.8	10.6	154600	US-09-949-016-1545	Sequence 14757, A
C 13	36.4	10.2	154600	US-09-949-016-1545	Sequence 14757, A
C 14	35.8	10.0	858	US-09-540-2361287	Sequence 1287, Appl
C 15	35.8	10.0	92407	US-09-596-007-56	Sequence 36, Appl
C 16	35.8	10.0	234884	US-09-949-016-16420	Sequence 16420, A
C 17	35.2	9.9	601	US-09-949-016-1645	Sequence 21645, A
C 18	35.2	9.9	601	US-09-949-016-156690	Sequence 156690, A
C 19	35.2	9.9	231129	US-09-949-016-16110	Sequence 16110, A
C 20	35.2	9.9	266293	US-09-949-016-1934	Sequence 11934, A
C 21	34.4	9.8	298	US-09-543-999C-10257	Sequence 10257, A
C 22	34.4	9.6	6588	US-09-949-016-1076	Sequence 1076, Appl
C 23	33.4	9.4	4438	US-09-949-016-13578	Sequence 13578, A
C 24	32.8	9.2	137753	US-09-949-016-17404	Sequence 17404, A

ALIGNMENTS

RESULT 1
99-09-526-193A-14

Sequence 14, Application US/09526193A
; GENERAL INFORMATION:
; PATENT NO. 6617122
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Pimstone, Simon N.
; TITLE OF INVENTION: CHOLESTEROL LEVELS
; FILE REFERENCE: 50110/002005
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FabSBQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 10545
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (1..(10545))
OTHER INFORMATION: n = a, t, c, or g
US-09-526-193A-14

Query Match. Best Local Similarity 98.9%; Pred. No. 2.5e-98; Mismatches 353; Conservative 0; Indels 1; Gaps 1;
Match 1 TGGAGGCTCACTGAGAGGGTGGATGAGTCCTCATGGTTATCTTGCGCTTGCGCA 60
Db 8043 TGGAGGCTCACTGAGAGGGTGGATGAGTCCTCATGGTTATCTTGCGCTTGCGCA 8102
Qy 61 ATAACTATGGCTGTCCCTCTGGTTATCTTGCGCTTGCGCA 120
Db 8103 ATAACTATGGCTGTCCCTCTGGTTATCTTGCGCTTGCGCA-GGGT 8161
Qy 121 CCCTGCTGTCAGCTCAGGCCCTGCCCTCCAGGGCTCCAGGCCACAGCCTGGCTGC 180

FILE REFERENCE: 91.US6.DIV
 CURRENT APPLICATION NUMBER: US/10/000,489
 PRIOR APPLICATION NUMBER: 2001-11-14
 PRIOR FILING DATE: 2001-08-06
 PRIORITY NUMBER: 1B01/01715
 PRIOR APPLICATION NUMBER: 2001-08-06
 PRIOR FILING DATE: 2001-05-25
 PRIORITY NUMBER: US 60/305,456
 PRIOR APPLICATION NUMBER: US 60/302,277
 PRIOR FILING DATE: 2001-07-13
 PRIORITY NUMBER: US 60/298,698
 PRIOR APPLICATION NUMBER: US 60/293,574
 PRIOR FILING DATE: 2001-06-15
 PRIORITY NUMBER: US 60/311,112
 SOFTWARE: JPatent
 SEQ ID NO: 101
 LENGTH: 1,062
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: 5' UTR
 NAME/KEY: polyA signal
 LOCATION: 1..153
 NAME/KEY: CDS
 LOCATION: 154..639
 NAME/KEY: 3' UTR
 LOCATION: 640..1,062
 NAME/KEY: polyA site
 LOCATION: 1,023..1,028
 LOCATION: 1,047..1,062

; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 14
 ; LENGTH: 10545

; TYPE: DNA
 ; ORGANISM: Homo sapiens

; FEATURE: misc_feature
 ; NAME/KEY: misc_feature
 ; LOCATION: (1) .. (10545)

; OTHER INFORMATION: n = a, t, c, or g
 US-09-526-193A-14

Query Match 89.4%; Score 142.2; DB 3; Length 10545;
 Best Local Similarity 97.5%; Pred. No. 1.3e-33;
 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 60
 Db 8142 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 8200

Query Match 89.4%; Score 142.2; DB 3; Length 10545;
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 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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Query Match 89.4%; Score 142.2; DB 3; Length 10545;
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 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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 Db 8142 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 8200

Query Match 89.4%; Score 142.2; DB 3; Length 10545;
 Best Local Similarity 97.5%; Pred. No. 1.3e-33;
 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 60
 Db 8142 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 8200

Query Match 89.4%; Score 142.2; DB 3; Length 10545;
 Best Local Similarity 97.5%; Pred. No. 1.3e-33;
 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 60
 Db 8142 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 8200

Query Match 89.4%; Score 142.2; DB 3; Length 10545;
 Best Local Similarity 97.5%; Pred. No. 1.3e-33;
 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 60
 Db 8142 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 8200

Query Match 89.4%; Score 142.2; DB 3; Length 10545;
 Best Local Similarity 97.5%; Pred. No. 1.3e-33;
 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 60
 Db 8142 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 8200

Query Match 89.4%; Score 142.2; DB 3; Length 10545;
 Best Local Similarity 97.5%; Pred. No. 1.3e-33;
 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 60
 Db 8142 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 8200

Query Match 89.4%; Score 142.2; DB 3; Length 10545;
 Best Local Similarity 97.5%; Pred. No. 1.3e-33;
 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 60
 Db 8142 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 8200

Query Match 89.4%; Score 142.2; DB 3; Length 10545;
 Best Local Similarity 97.5%; Pred. No. 1.3e-33;
 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 60
 Db 8142 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 8200

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Query Match 89.4%; Score 142.2; DB 3; Length 10545;
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Query Match 89.4%; Score 142.2; DB 3; Length 10545;
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Query Match 89.4%; Score 142.2; DB 3; Length 10545;
 Best Local Similarity 97.5%; Pred. No. 1.3e-33;
 Matches 155; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 60
 Db 8142 TTAATGACAGCCACGGGCCTCCCTGTAGCTTCGGCGTCCC 8200

Qy	22.09	TCCCTCTGAGGACCTGGGGAGCTCAGGCTGGGGATCTCCAGGCCATGTTAGGTCCCTATCA	22.68
Db	4.12	TCCCTCTGAGGACCTGGGGAGCTCAGGCTGGGGATCTCCAGGCCATGTTAGGTCCCTATCA	4.71
Qy	22.69	AATATCAAGTCAGGTTGTGGGGAAAACAAGAGGCCATTACCAAGGACTGT	23.28
Db	472	AATATCAAGTCAGGTTGTGGGGAAAACAAGAGGCCATTACCAAGGACTGT	5.31
Qy	23.29	CGCCCTTCCCTCACCCAGCTTAGGCCCTTGAAAGAACAAAGAACAAAGAACAAATGA	23.88
Db	532	CGCCCTTCCCTCACCCAGCTTAGGCCCTTGAAAGAACAAAGAACAAATGA	5.91
Qy	23.89	TTRGGCTCTGAGGGAGATTCAAGCTTCAAGCTTCTCTCCCATTCCTCCCTCCGCCT	24.48
Db	592	TTRGGCTCTGAGGGAGATTCAAGCTTCAAGCTTCTCTCCCATTCCTCCGCCT	6.50
Qy	24.49	GAGGAAGCTAACAAAGGAAAAAAATTGCGAAAGCAGGATTAGAGAAGCTGAGCTTAC	25.08
Db	651	GAGGAAGCTAACAAAGGAAAAAAATTGCGAAAGCAGGATTAGAGAAGCTGAGCTTAC	7.10
Qy	25.09	ACTGGTGCCTTGGTGCGGGAACGTGCTAGAAGACTGAGCTAGAAGACTCTGGCG	25.68
Db	711	ACTGGTGCCTTGGTGCAGGACTGAGCTAGAAGACTCTGGCG	7.70
Qy	25.69	AGCGCTTCCGGCGCTTCTAGCGGGCGGCCGGGGAGGGAGCGAGCGCG	26.28
Db	771	AGCGCTTCCGGCGCTTCTAGCGGGCGGCCGGGGAGGGAGCGAGCGCG	8.30
Qy	26.29	GAACCTTAAGACACCTGCTGTACCCCTAACCCCCACCCACCTCCCCAAC	26.88
Db	831	GAACCTTAAGACACCTGCTGTACCCCTAACCCCCACCTCCCCAAC	8.85
Qy	26.89	TCCCTCTAGATGTCGTCGTCGGGGCTGAACTGTCGCGGTTAACGGCG	27.48
Db	886	TCCCTCTAGATGTCGTCGTCGGGGCTGAACTGTCGCGGTTAACGGCG	9.45
Qy	27.49	CCTGGCTTCTGCTGAACTGACTCATATAACAGGCGGAAAGGGGGGGGG	28.08
Db	946	CCTGGCTTCTGCTGAACTGACTCATATAACAGGCGGAAAGGGGGGGGG	10.05
Qy	28.09	GGGAGAGCACAGCCTTGACCGATAATGTAACCCTGCTGGCTGGCTGG	28.68
Db	1006	GGGAGAGCACAGCCTTGACCGATAATGTAACCCTGCTGGCTGGCTGG	10.65
Qy	28.69	AGGAACATGTCGGGAAACCCGTAATTGCGAGGCGAGTGTGGGGGGGG	29.28
Db	1066	AGGAACATGTCGGGAAACCCGTAATTGCGAGGCGAGTGTGGGGGGGG	11.25
Qy	29.29	GGAGAGCGGAGCCCTTCTCCAGGGCTGCGCAAGGGGGGGGGCTCGCG	29.88
Db	1126	GGAGAGCGGAGCCCTTCTCCAGGGCTGCGCAAGGGGGGGCTCGCG	11.85
Qy	29.89	CACCAACAGAGC 3000	
Db	1186	CACCAACAGAGC 1197	

RESULT 4
US-09-944-116-17196
; Sequence 17136, Application 1670949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: CLO01307
; FIVE REFERENCE: CURRENT APPLICATION NUMBER: US/09/944-116

